

## CLAIM AMENDMENTS

1. (currently amended) A method for detecting the presence or absence of a *Campylobacter* strain selected from the group consisting of *C. jejuni*; *C. coli*; *C. lari*; *C. upsaliensis*; *C. fetus* spp *fetus* and mixtures thereof in a sample comprising:

adding the sample to an amplification mix including at least one primer pair selected from the group consisting of: at least 15 contiguous nucleotides of: ACTTCTTTATTGCTTGCTGC (SEQ ID NO. 1) and at least 15 contiguous nucleotides of GCCACAACAAGTAAAGAAGC (SEQ ID NO. 2); and at least 15 contiguous nucleotides of GTAAAACCAAAGCTTATCGTG (SEQ ID NO. 3) and at least 15 contiguous nucleotides of TCCAGCAATGTGTGCAATG (SEQ ID NO. 4); TAGAGAGATAGCAAAAAGAGA (SEQ ID NO. 5) and TAGACATAATAATCCGACCC (SEQ ID NO. 6); AATTGAAACTCTTGCTATCG (SEQ ID NO. 7) and TCATACATTTACCGGAGCT (SEQ ID NO. 8); GCAAAATATAAATGTAAGCGGAGAG (SEQ ID NO. 9) and TGCAGCGCGCCGACCTAT (SEQ ID NO. 10); TATACCGGTAAGGAGTGCTGGAG (SEQ ID NO. 11) and ATCAATTAACCTTCGAGCACCG (SEQ ID NO. 12);

incubating the amplification mixture under conditions promoting nucleic acid amplification; and

detecting the amplification product.

2. (currently amended) A pair of amplification primers selected from the group consisting of: at least 15 contiguous nucleotides of: ACTTCTTTATTGCTTGCTGC (SEQ ID NO. 1) and at least 15 contiguous nucleotides of GCCACAACAAGTAAAGAAGC (SEQ ID NO. 2); and at least 15 contiguous nucleotides of GTAAAACCAAAGCTTATCGTG (SEQ ID NO. 3) and

at least 15 contiguous nucleotides of TCCAGCAATGTGTGCAATG (SEQ ID NO. 4); TAGAGAGATAGCAAAAGAGA (SEQ ID NO. 5) and TACACATAATAATCCGACCC (SEQ ID NO. 6); AATTGAAACTCTTGCTATGC (SEQ ID NO. 7) and TCATACATTTTACCCGAGCT (SEQ ID NO. 8); GCAAAATATAAATGTAAGCGGAGAG (SEQ ID NO. 9) and TGCAGCGGGCCGACCTAT (SEQ ID NO. 10); TATACCGGTAAGGAGTGCTGGAG (SEQ ID NO. 11) and ATCAATTAACCTTCGAGCACCG (SEQ ID NO. 12); and mixtures thereof.

3. (currently amended) A kit comprising at least one primer selected from the group consisting of: at least 15 contiguous nucleotides of: ACTTCTTTATTGCTTGCTGC (SEQ ID NO. 1) and at least 15 contiguous nucleotides of GCCACAACAAGTAAAGAAGC (SEQ ID NO. 2); and at least 15 contiguous nucleotides of GTAAACCAAAGCTTATCGTG (SEQ ID NO. 3) and at least 15 contiguous nucleotides of TCCAGCAATGTGTGCAATG (SEQ ID NO. 4); TAGAGAGATAGCAAAAGAGA (SEQ ID NO. 5) and TACACATAATAATCCGACCC (SEQ ID NO. 6); AATTGAAACTCTTGCTATGC (SEQ ID NO. 7) and TCATACATTTTACCCGAGCT (SEQ ID NO. 8); GCAAAATATAAATGTAAGCGGAGAG (SEQ ID NO. 9) and TGCAGCGGGCCGACCTAT (SEQ ID NO. 10); TATACCGGTAAGGAGTGCTGGAG (SEQ ID NO. 11) and ATCAATTAACCTTCGAGCACCG (SEQ ID NO. 12) and mixtures thereof.